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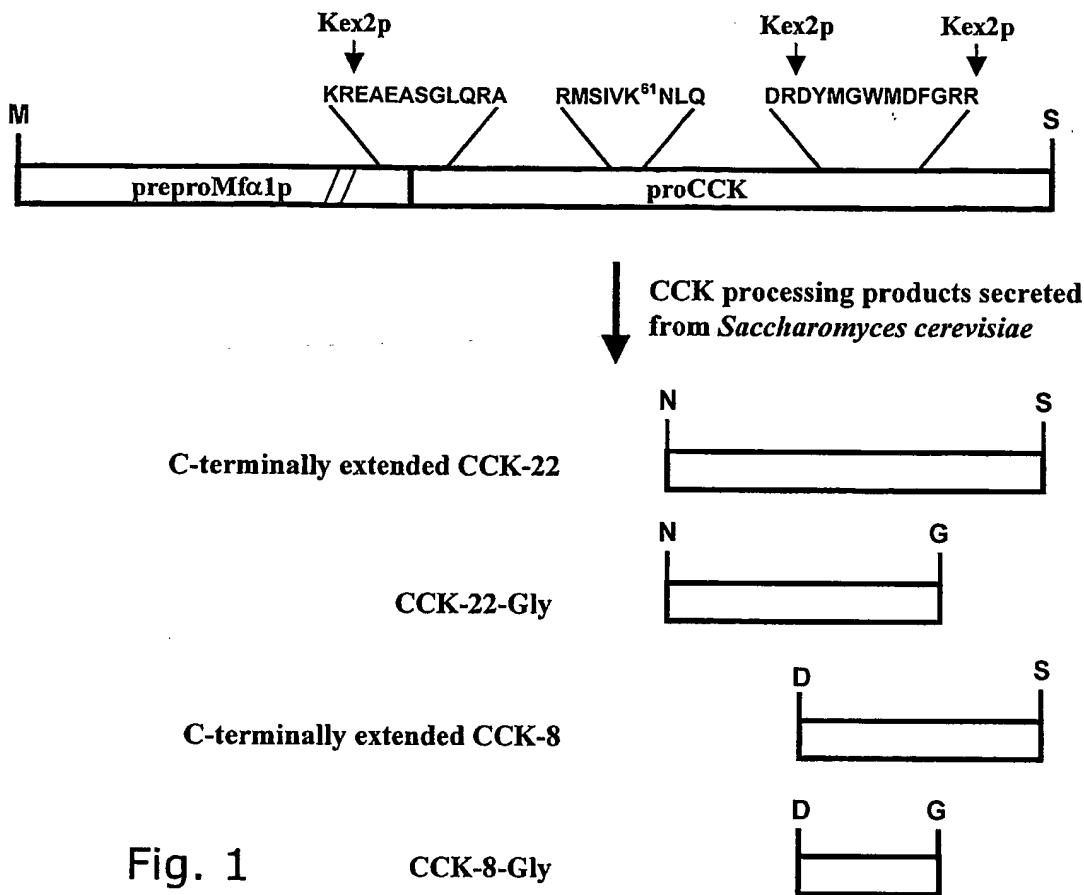


Fig. 1

CCK-8-Gly

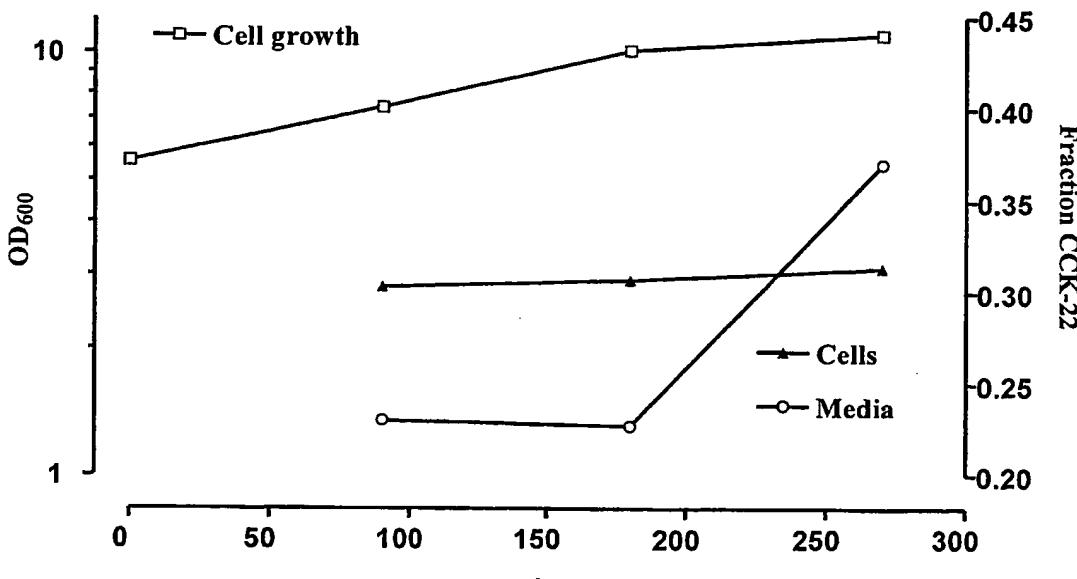
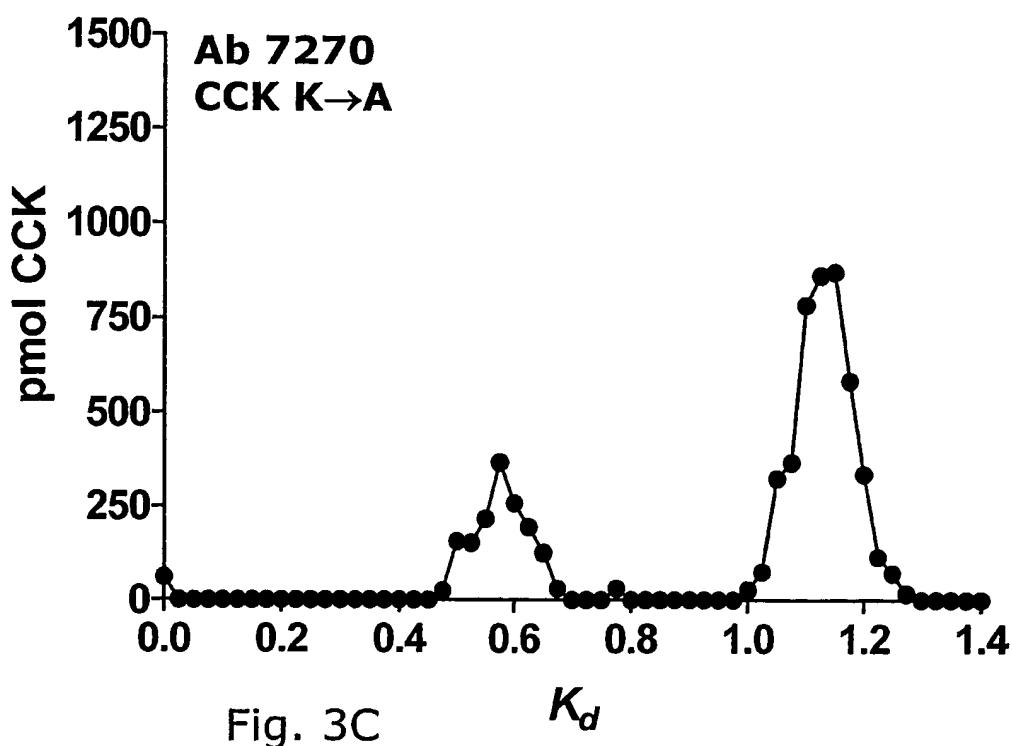
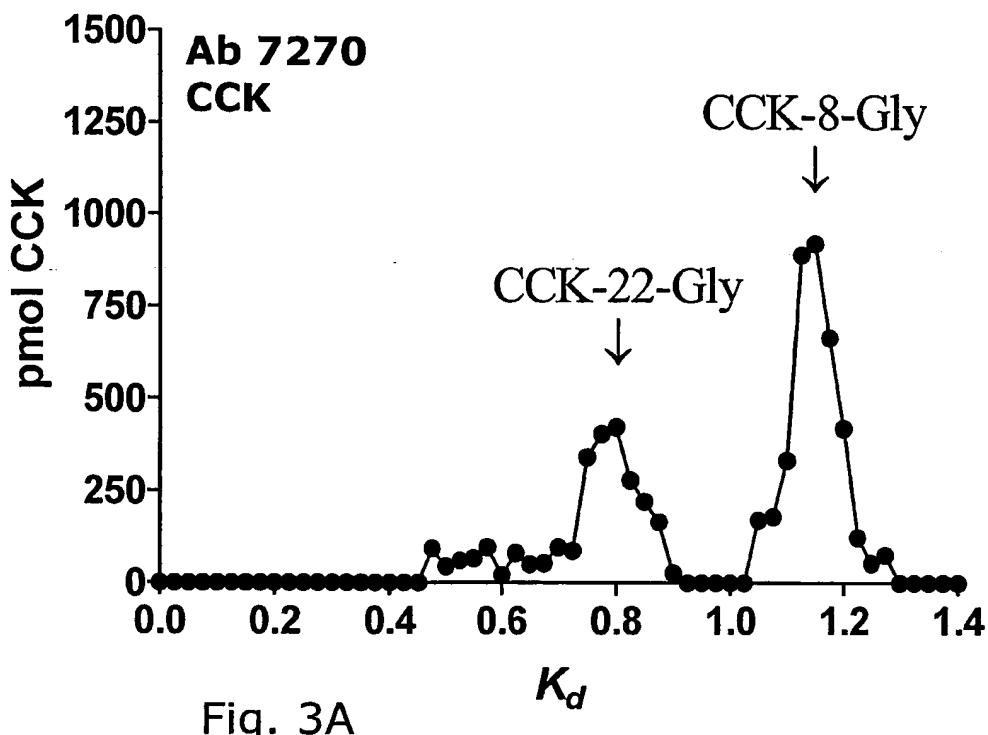


Fig. 2

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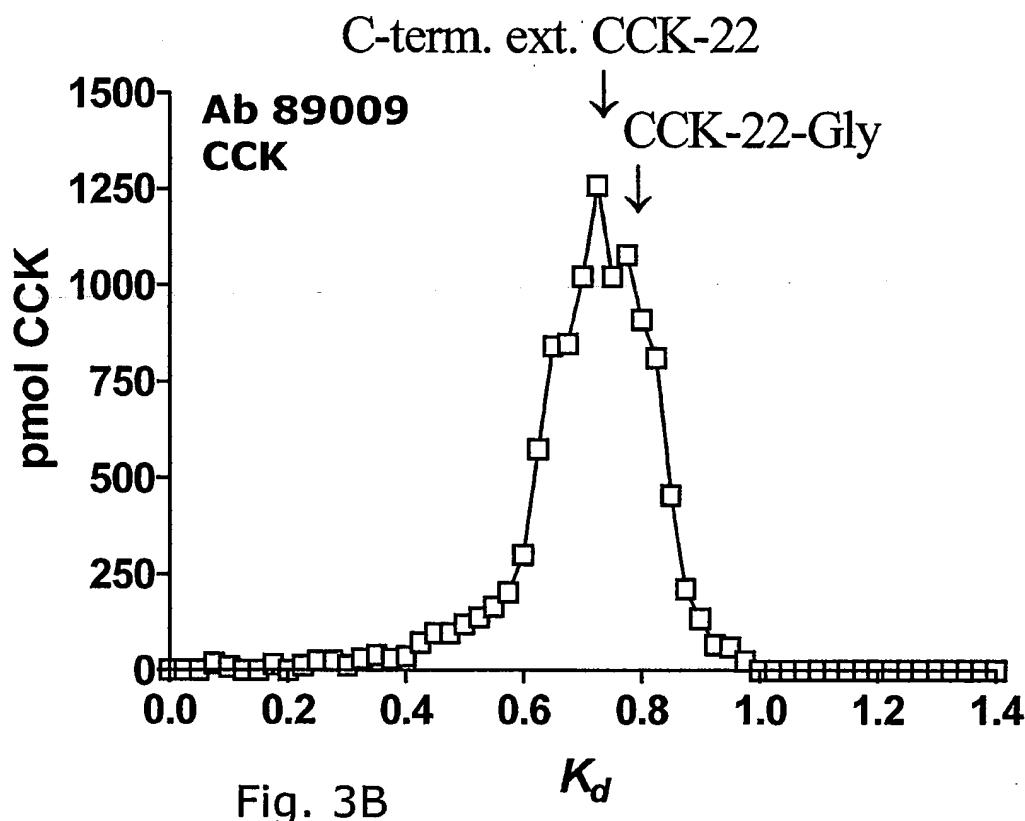


Fig. 3B

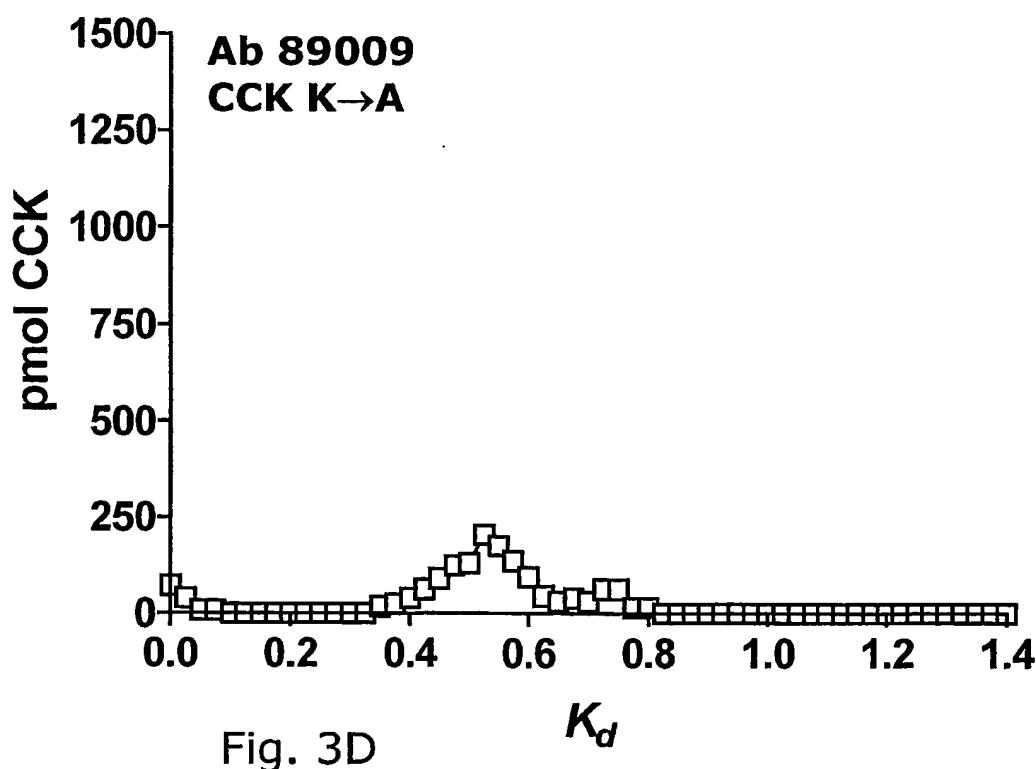
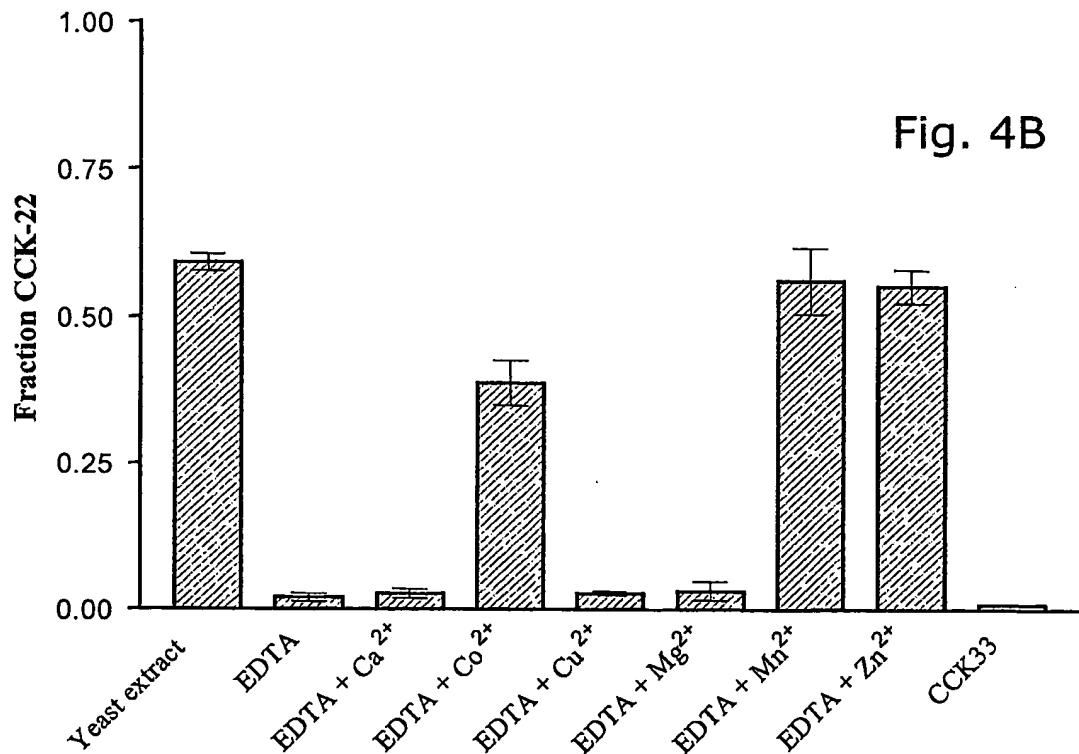
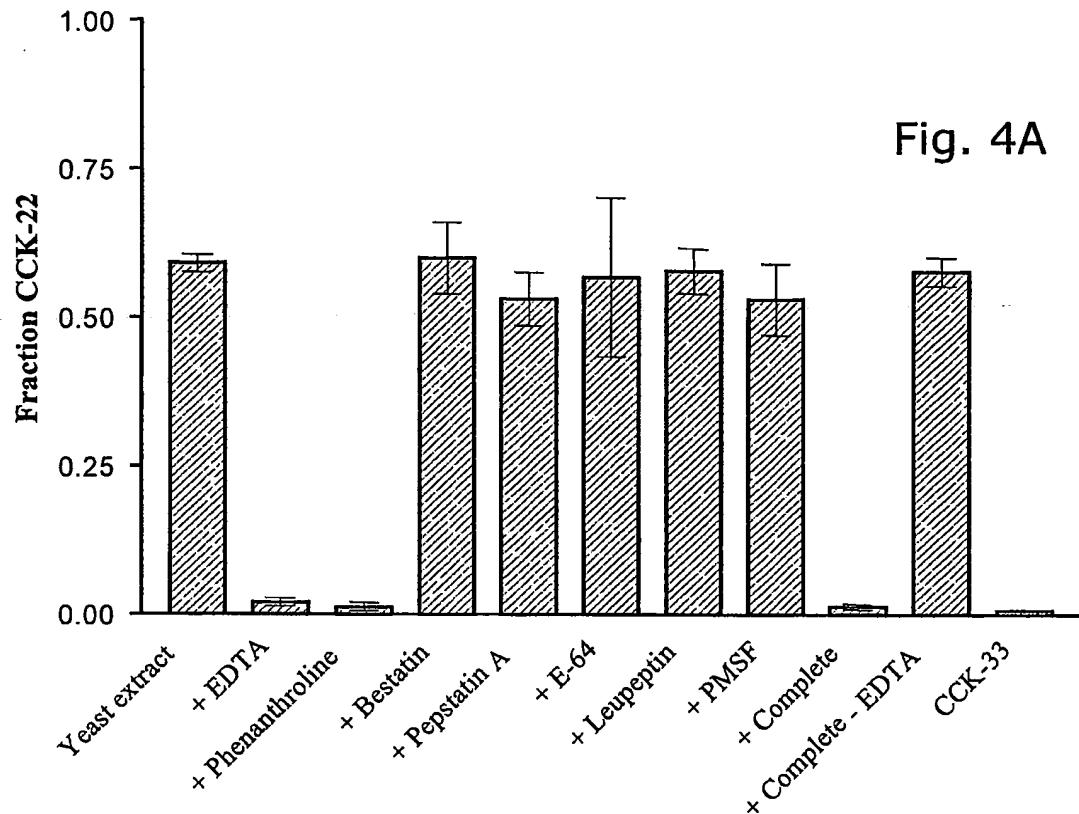


Fig. 3D

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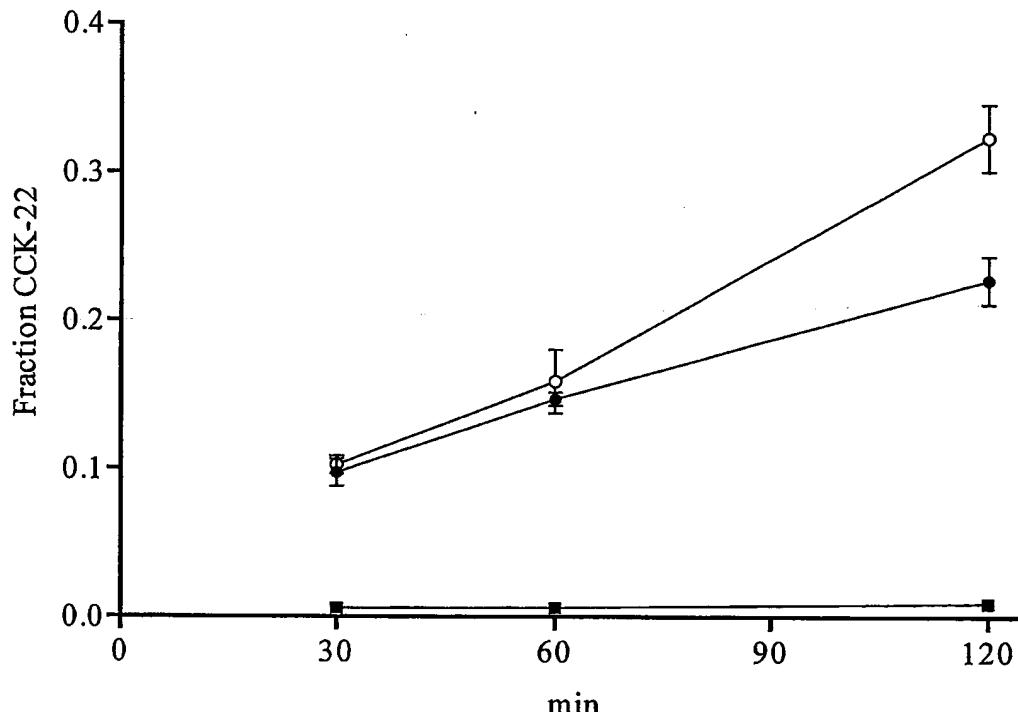


Fig. 5

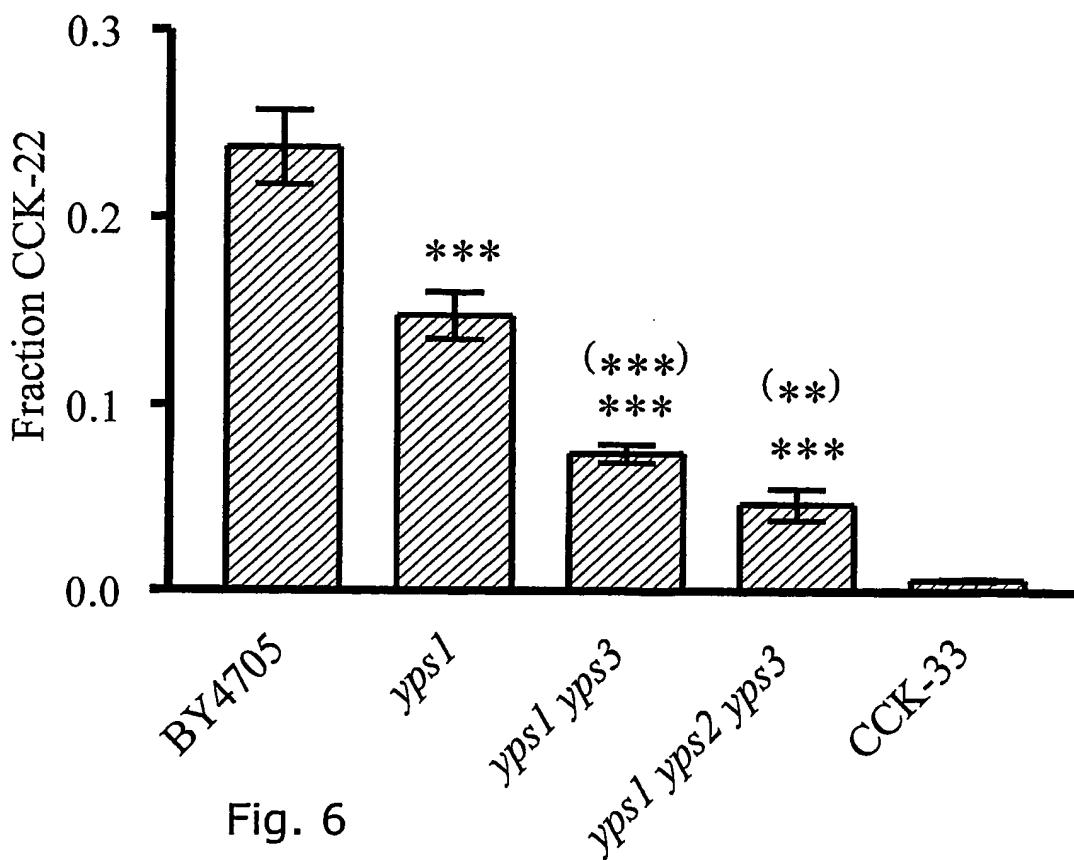
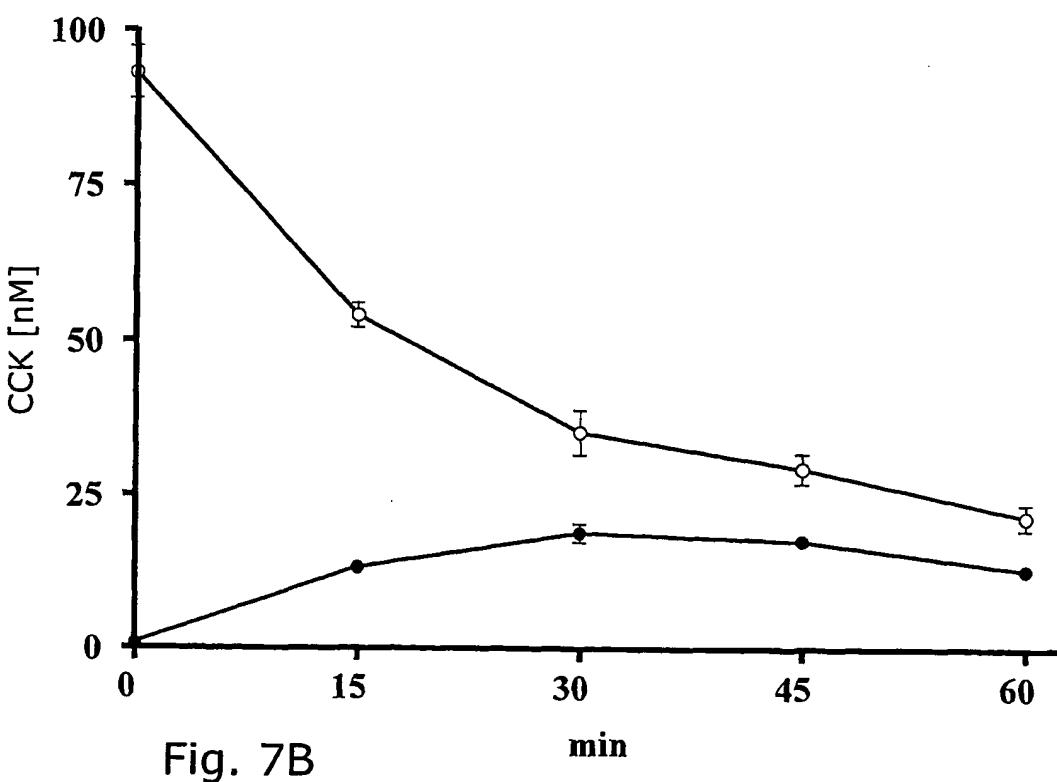
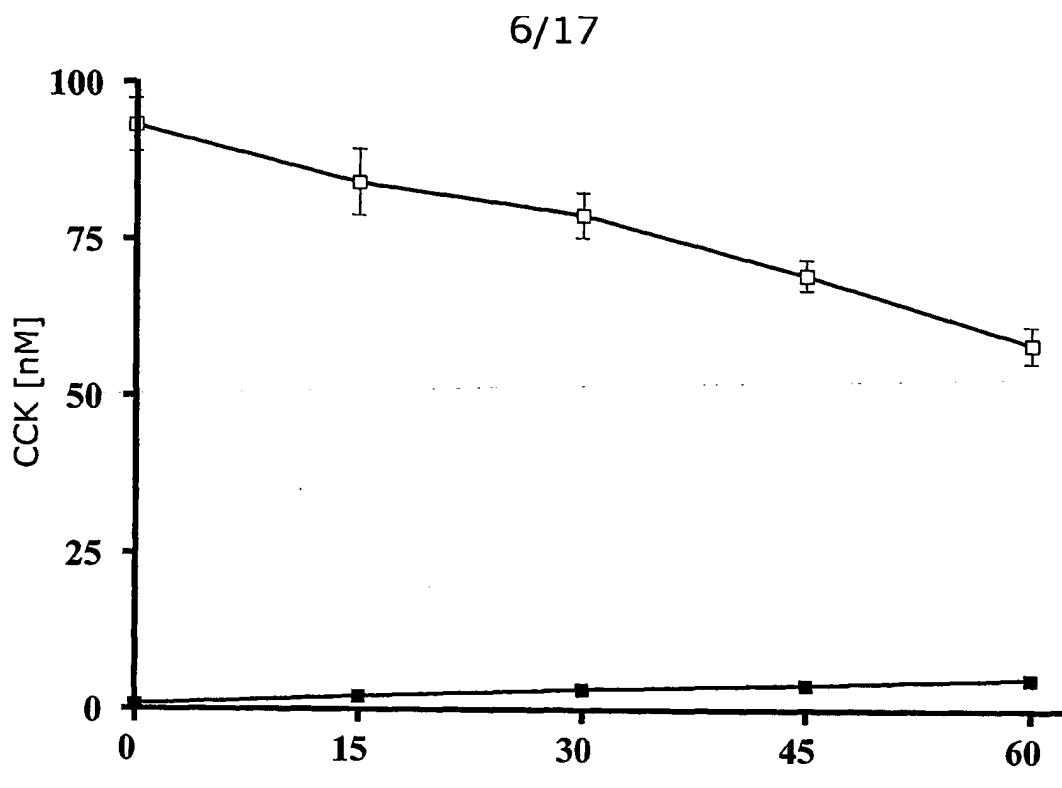


Fig. 6



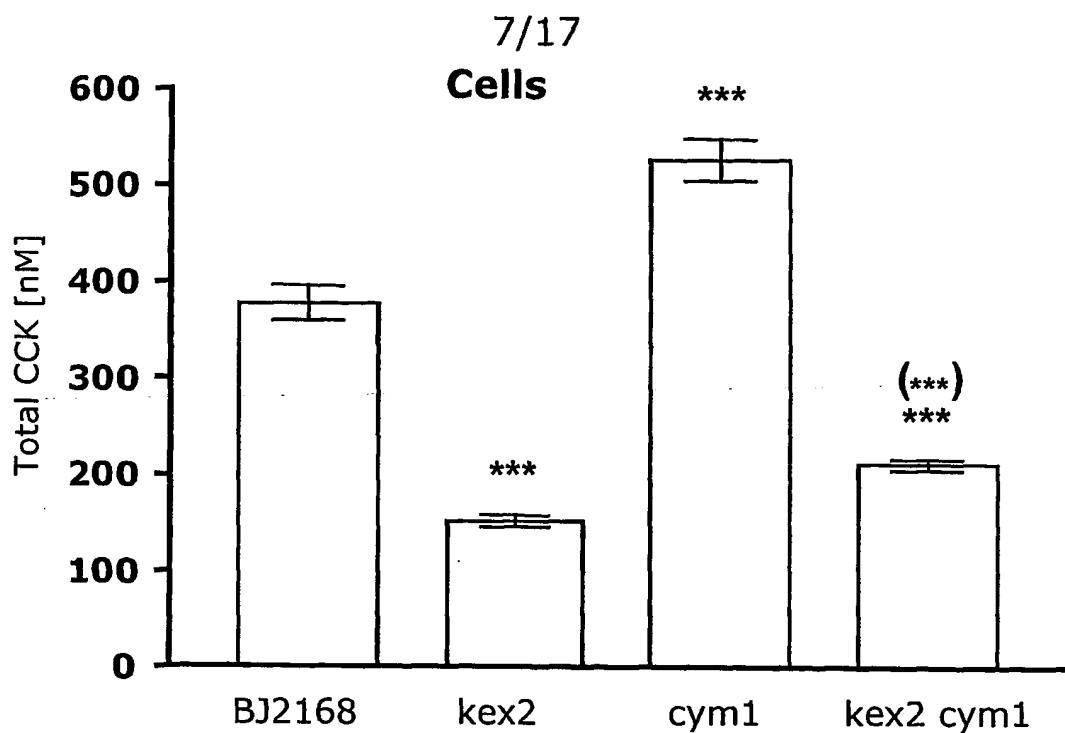


Fig. 8A

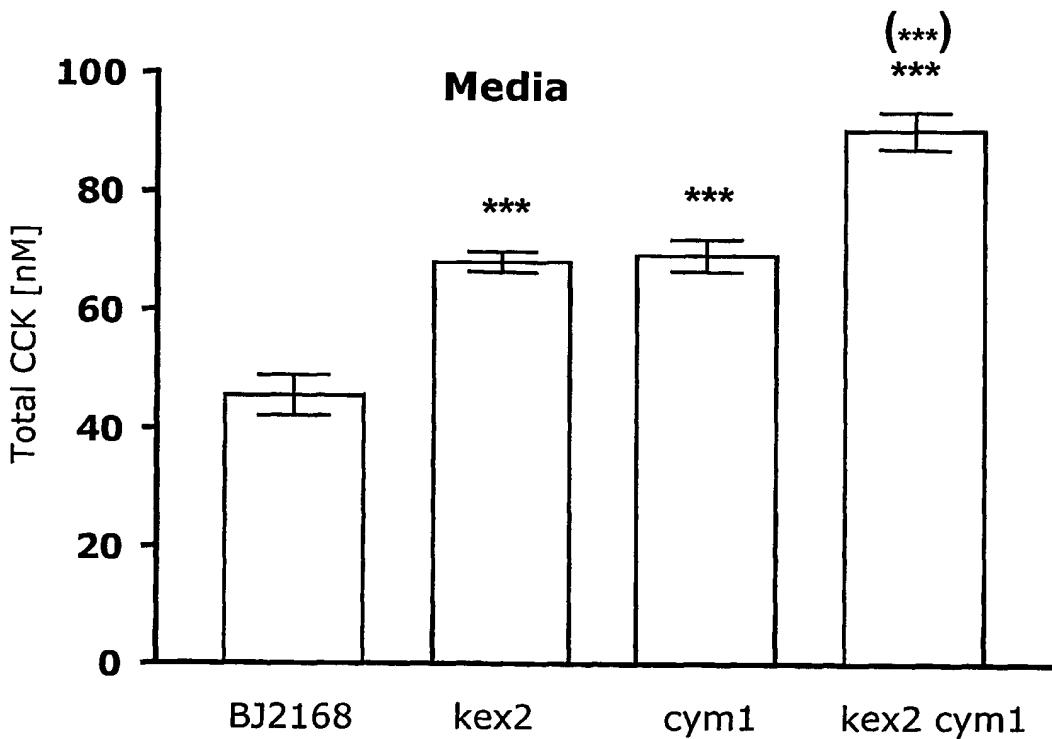


Fig. 8B

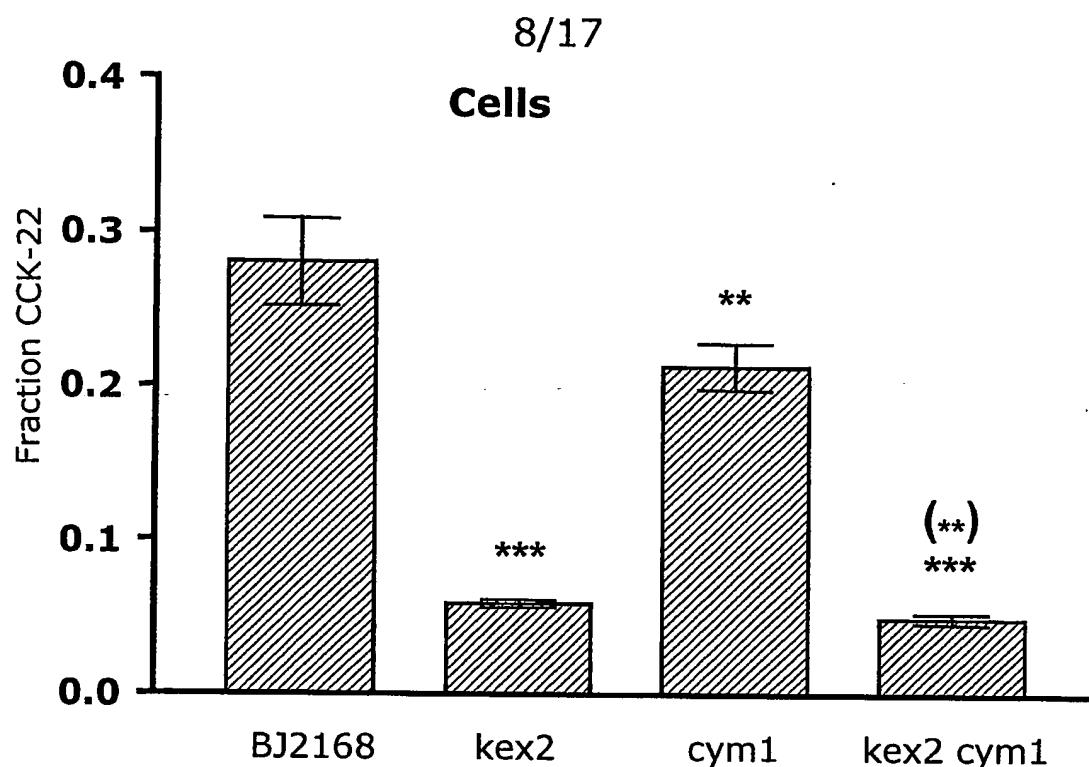


Fig. 8C

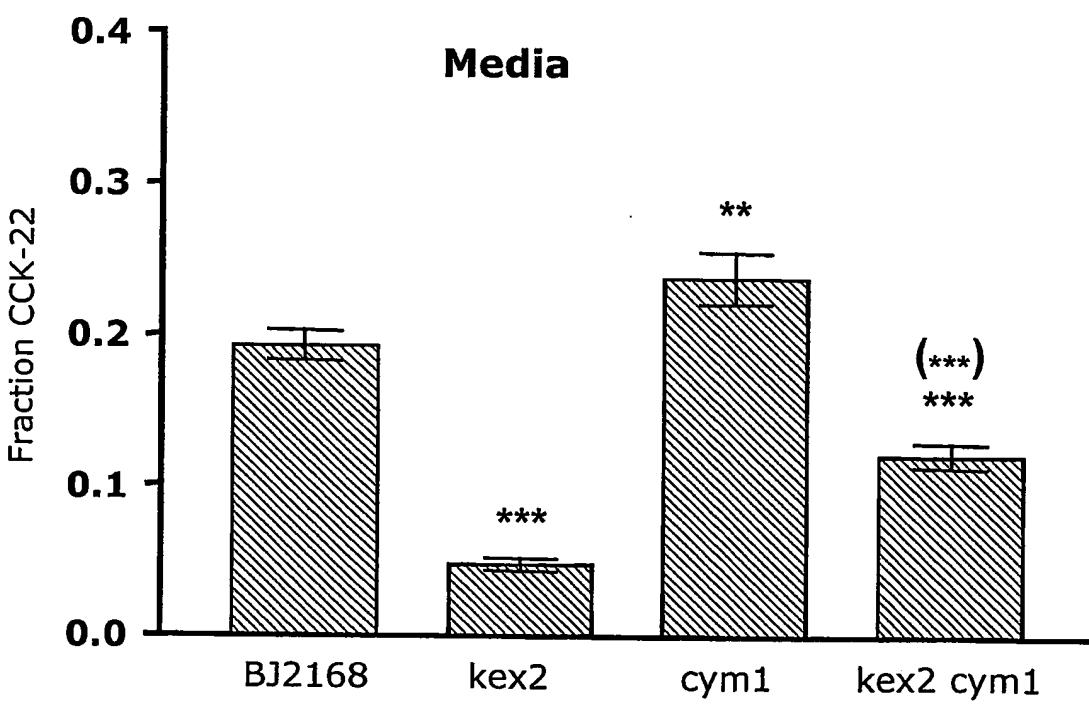


Fig. 8D

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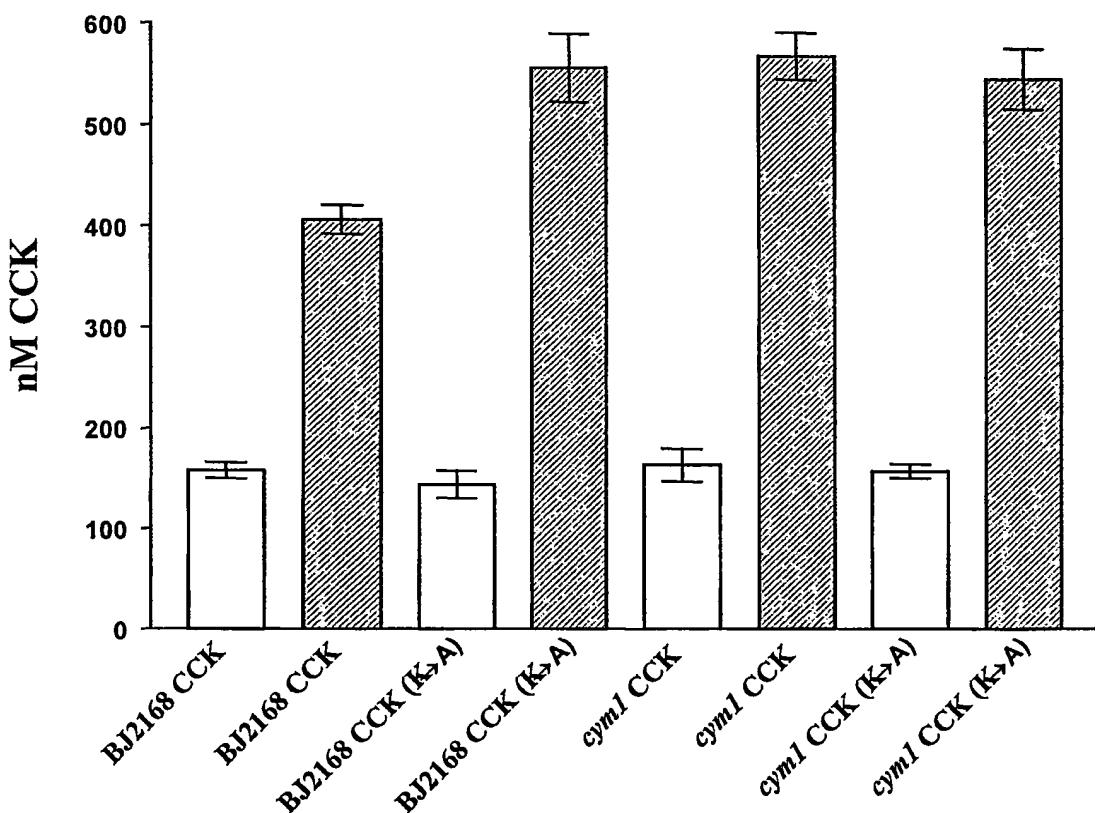
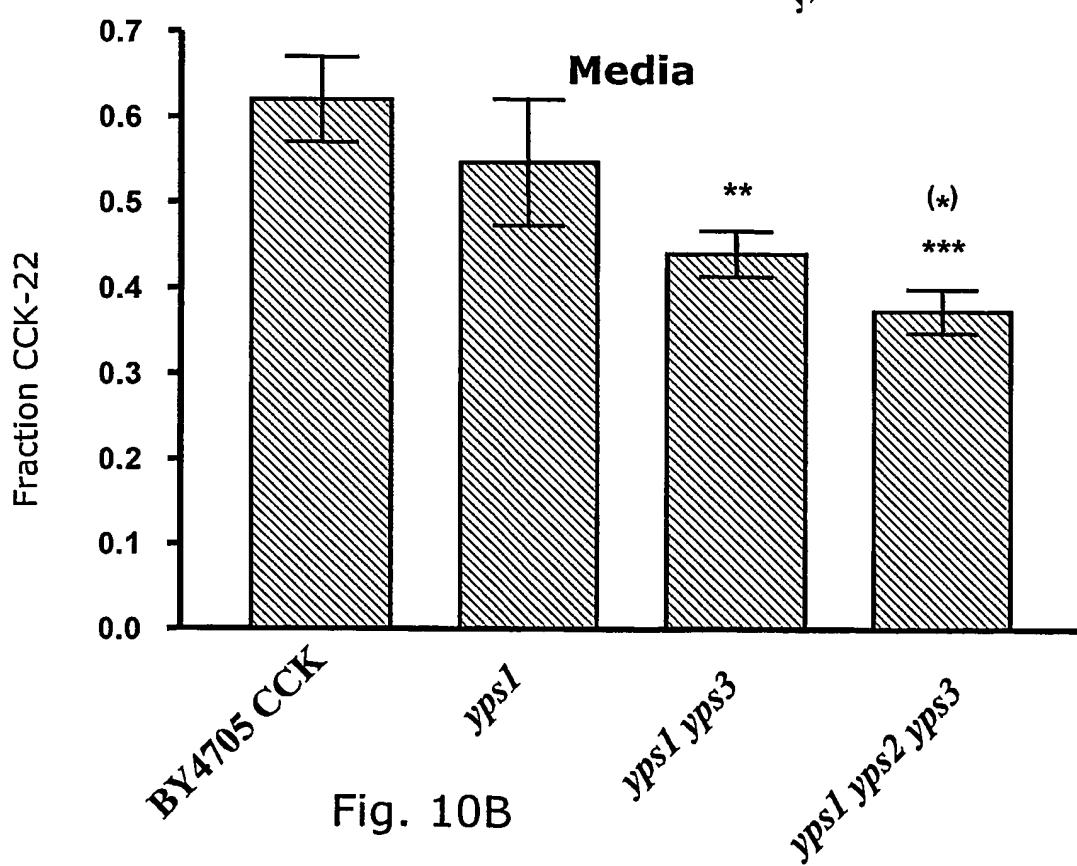
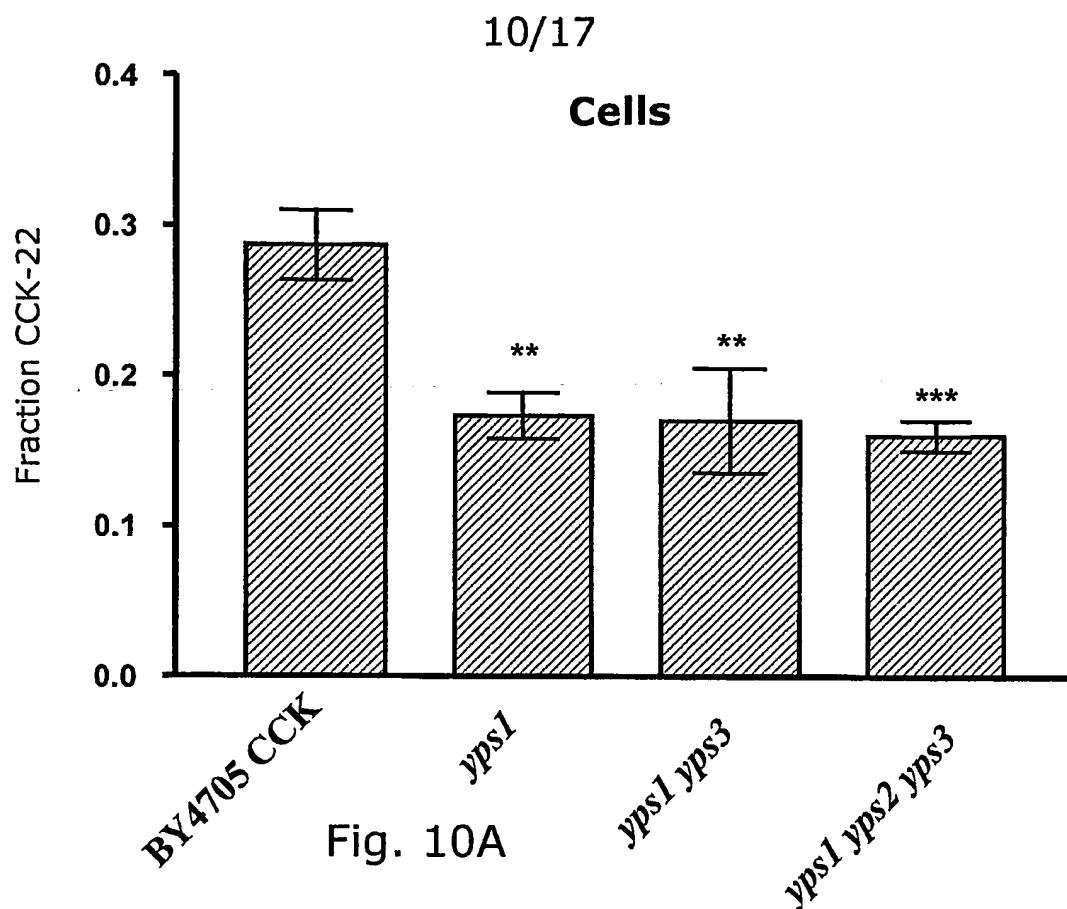
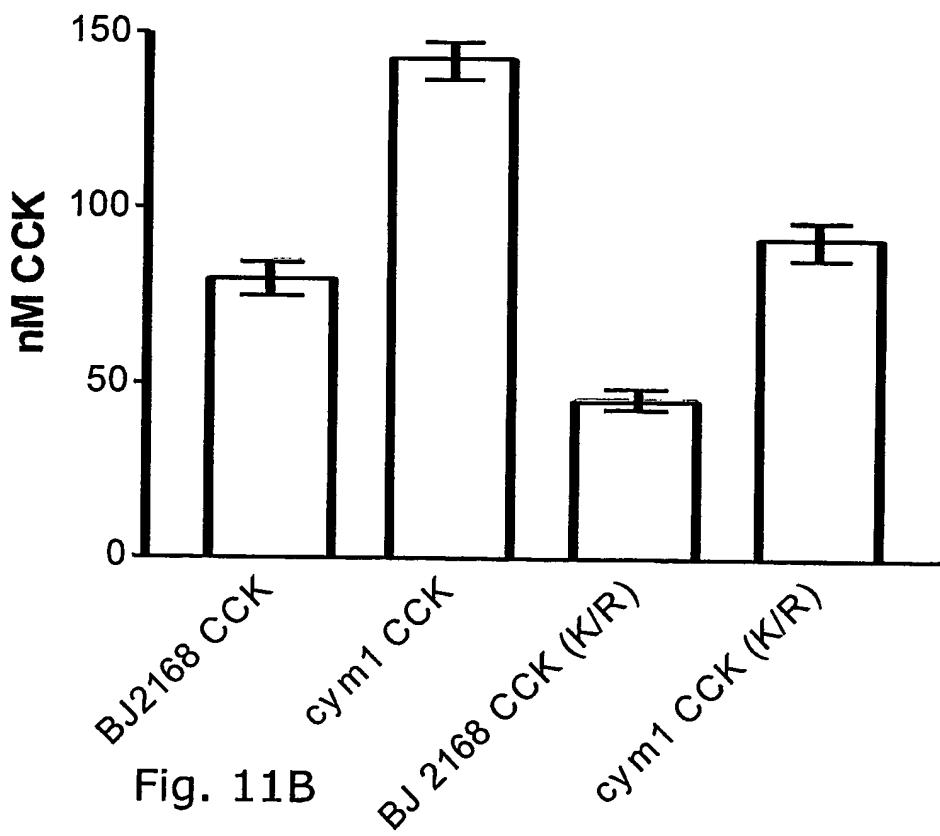
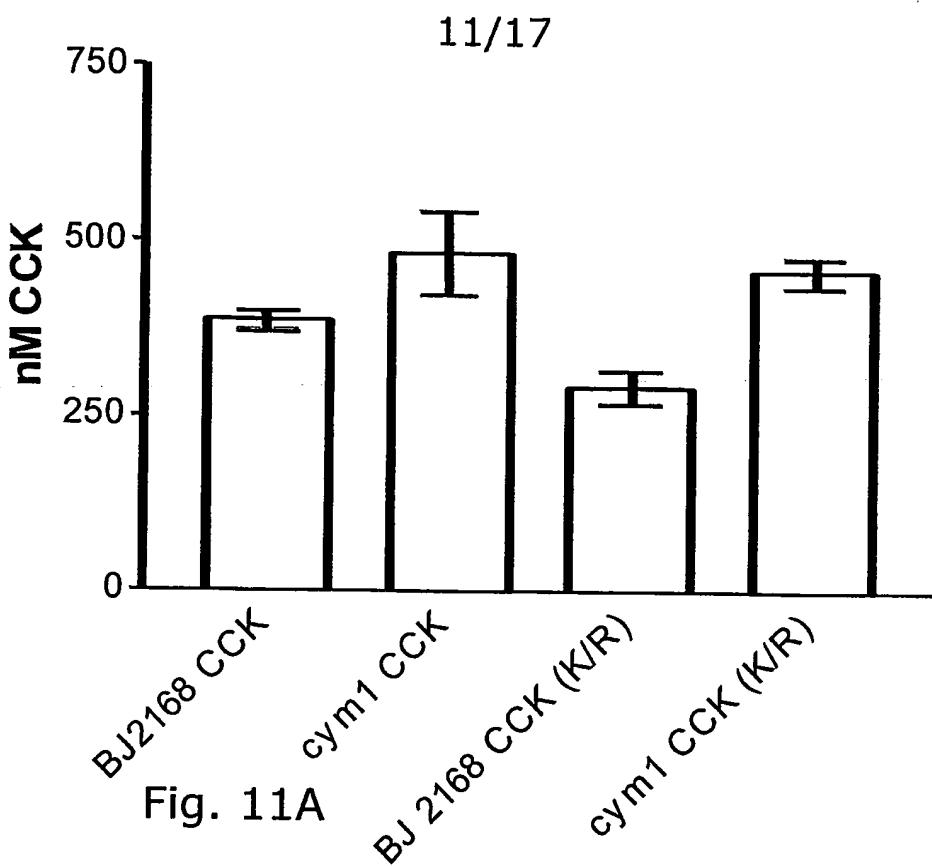


Fig. 9





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<u>ProCCK</u>		<u>Molecular mass</u>	<u>Strain</u>	<u>SEQ ID NO.</u>
CCK-61	CCK-58	CCK-39	CCK-22	CCK-8
PreproM <sup>alpha</sup> 1p	//. SGLQRATEAPRQLRVSQRTDGESERAHIGALLARYTQQARRAPSGRMSIVKNLQNLDPSPHRISDRDYMGMWMDFGRRSAEEYEYPPS			43
	QIRVSQLRTDGESERAHIGALLAR			
	VSQRTDGESERAHIGALLAR			
		2433.3	2433.5	B 44
		2036.1	2036.1	B 45
	YIQQARKAPSGRMSIVKNLQNLDPSPHRISDRDYMGMWMDFGRRSAEEYEYPPS	6051.9*	6051.6*	B 46
	YIQQARKAPSGRMSIVK	1932.1	1932.2	A & B 47
	YIQQARKAPSGRMSIVK	1805.2	1805.0	A 48
	NLQNLDPSPHRISD	1509.0	1508.7	A 49
	NLQNLDPSPHRISDRDYMGMWMDFG	2766.2	2766.1	A 50
	NLQNLDPSPHRISDRDYMGMWMDFGRRSAEEYEYPPS	4133.8	4133.9	A & B 51
	DYMGWMDFGRSAEEYEYPPS	2488.0	2488.1	A 52

Fig. 12

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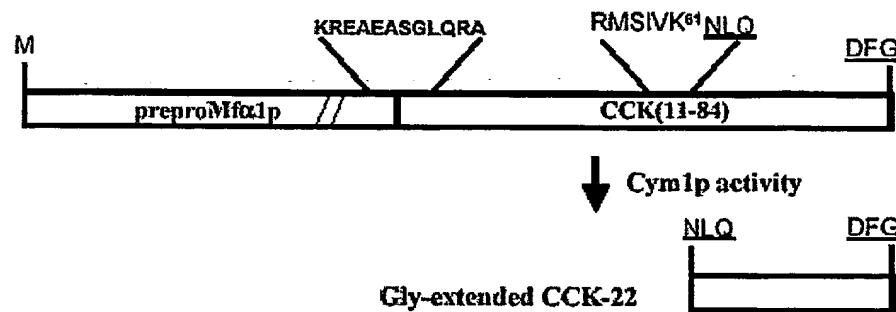


Fig. 13A

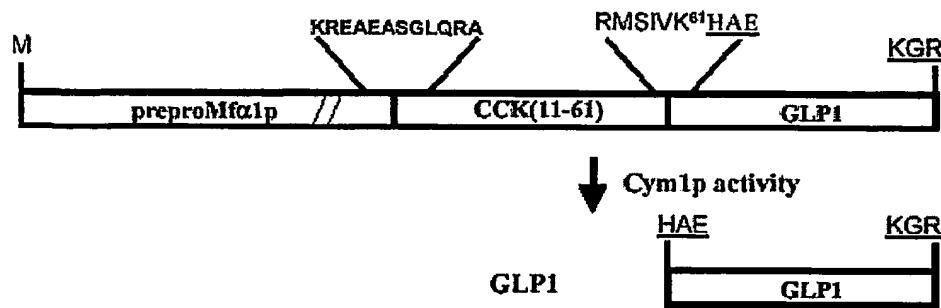


Fig. 13B

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ATGAGATTCCTCAATTTACTGCAGTTATCGCAGCATCCTCCGCATTAGCTGCT  
1 -----+-----+-----+-----+-----+-----+ 60  
TACTCTAAAGGAAGTAAAAATGACGTAAAATAAGCGTCGTAGGAGGCGTAATCGACGA  
M R F P S I F T A V L F A A S S A L A A -  
  
CCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCACTGGT  
61 -----+-----+-----+-----+-----+-----+ 120  
GGTCAGTTGTATGTTGTCTTCTACTTGCCGTGTTAAGGCCGACTTCGACAGTAGCCA  
P V N T T E D E T A Q I P A E A V I G -  
  
TACTTAGATTTAGAAGGGGATTCGATGTTGCTGTTGCCATTTCACAGCACAAAT  
121 -----+-----+-----+-----+-----+-----+ 180  
ATGAATCTAAATCTTCCCCTAAAGCTACAACGACAAACGGTAAAGGTTGTCGTGTTA  
Y L D L E G D F D V A V L P F S N S T N -  
  
AACGGGTTATTGTTATAAATACTACTATTGCCAGCATTGCTGCTAAAGAAGAAGGGTA  
181 -----+-----+-----+-----+-----+-----+ 240  
TTGCCCAATAACAAATATTATGATGATAACGGTCGTAACGACGATTTCTTCTTCCCCT  
N G L L F I N T T I A S I A A K E E G V -  
  
TCTTTGGATAAAAGAGAGGCTGAAGCTCACCGCTGGCAGCCCCGGTCAGCCTCGGAC  
241 -----+-----+-----+-----+-----+-----+ 300  
AGAAACCTATTTCTCTCCGACTTCGAGTGGCGACCCGTGGGGCCAAGTCGGAGCCTG  
S L D K R E A E A H P L G S P G S A S D -  
  
TTGGAAACGTCCGGGTTACAGGAGCAGCGCAACCATTGCAGGGCAAACGTGGAGCTG  
301 -----+-----+-----+-----+-----+-----+ 360  
AACCTTGCAAGGCCAATGTCCTCGTCGCGTTGGTAAACGTCCGTTGACAGCCTCGAC  
L E T S G L Q E Q R N H L Q G K L S E L -  
  
CAGGTGGAGCAGACATCCCTGGAGCCCCCTCCAGGAGAGCCCCCGTCCCACAGGTGTCTGG  
361 -----+-----+-----+-----+-----+-----+ 420  
GTCCACCTCGTCTGTAGGGACCTCGGGGAGGTCTCTCGGGGGCAGGGTGTCCACAGACC  
Q V E Q T S L E P L Q E S P R P T G V W -  
  
AAGTCCCGGGAGGTAGCCACCGAGGGCATCCGTGGCACCGCAAAATGGCCTCTACACC  
421 -----+-----+-----+-----+-----+-----+ 480  
TTCAGGGCCCTCCATCGGTGGCTCCCGTAGGCACCCGTGGCGTTTACCAAGGAGATGTGG  
K S R E V A T E G I R G H R K M V L Y T -  
  
CTGGGGCACCACGAAGCCCCAAGATGGTCAAGGGTCTGGCTGCTTGGGAGGAAGATG  
481 -----+-----+-----+-----+-----+-----+ 540  
GACGCCCGTGGTGGCTTCGGGTTCTACACAGTCCAGACCGACGAAACCCCTCTAC  
L R A P R S P K M V Q G S G C F G R K M -  
  
GACCGGATCAGCTCCTCCAGTGGCCTGGCTGCAAAGTGTGAGGGCGGCAATTAA  
541 -----+-----+-----+-----+-----+-----+ 594  
CTGGCCTAGTCGAGGGAGGTACCGGACCCGACGTTTACGACTCCGCCGTAATT  
D R I S S S S G L G C K V L R R H \* -

Fig. 14A

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ATGAGATTCCTCAATTTACTGCAGTTATCGCAGCATCCTCCGCATTAGCTGCT  
 1 -----+-----+-----+-----+-----+-----+ 60  
 TACTCTAAAGGAAGTTAAAAATGACGTCAAAATAAGCGTCTAGGAGGCGTAATCGACGA  
 M R F P S I F T A V L F A A S S A L A A -  
 CCAGTCAACACTACAACAGAACAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCATCGGT  
 61 -----+-----+-----+-----+-----+-----+ 120  
 GGTCAGTTGTGATGTTCTACTTGCCTGTTAAGGCCGACTTCGACAGTAGCCA  
 P V N T T T E D E T A Q I P A E A V I G -  
 TACTTAGATTTAGAAGGGGATTCGATGTTGCTGTTGCCATTCCAACAGCACAAAT  
 121 -----+-----+-----+-----+-----+-----+ 180  
 ATGAATCTAAATCTCCCTAAAGCTACAACGACAAACGGTAAAGGTTGTCGTGTTA  
 Y L D L E G D F D V A V L P F S N S T N -  
 AACGGGTTATTGTTATAAATACTACTATTGCCAGCATTGCTGCTAAAGAAGAAGGGTA  
 181 -----+-----+-----+-----+-----+-----+ 240  
 TTGCCCAATAACAAATATTATGATGATAACGGTCGTAACGACGATTCTCTCCCAT  
 N G L L F I N T T I A S I A A K E E G V -  
 TCTTGATAAAAGAGAGGGCTGAAGCTAGCCCCAAGATGGTGCAAGGGCTGGCTGCTT  
 241 -----+-----+-----+-----+-----+-----+ 300  
 AGAAACCTATTTCTCTCCACTTCGATGGGTTCTACCACGTTCCAGACGACGAAA  
 S L D K R E A E A S P K M V Q G S G C F -  
 GGGAGGAAGATGGACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGG  
 301 -----+-----+-----+-----+-----+-----+ 360  
 CCCTCCCTCTACCTGGCCTAGTCGAGGAGGTACCGGACCCGACGTTACGACTCCGCC  
 G R K M D R I S S S S G L G C K V L R R -  
 CATTAA  
 361 ----- 366  
 GTAATT  
 H \* -

Fig. 14B

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1 ATGAGATTCCTCAATTTACTGCAGTTATTGCAGCATCCTCCGCATTAGCTGCT 60  
 1 TACTCTAAAGGAAGTTAAAATGACGTCAAAATAAGCGTCGTAGGAGGCATAATCGACGA  
 M R F P S I F T A V L F A A S S A L A A -  
 61 CCAGTCAACACTACAACAGAAGATGAAACGGCACAAATTCCGGCTGAAGCTGTCACTCGGT 120  
 61 GGTCAGTTGTGATGTTGTCTTCTACTTGCCTGTTAAGGCCGACTTCGACAGTAGCCA  
 P V N T T T E D E T A Q I P A E A V I G -  
 121 TACTTAGATTTAGAAGGGGATTCGATGTTGCTGTTGCCATTCCAAACAGCACAAAT 180  
 121 ATGAATCTAAATCTTCCCCTAAAGCTACAACGACAAACGGTAAAGGTTGTCGTGTTA  
 Y L D L E G D F D V A V L P F S N S T N -  
 181 AACGGGTTATTGTTATAAATACTACTATTGCCAGCATTGCTGCTAAAGAAGAAGGGTA 240  
 181 TTGCCCAATAACAAATATTATGATGATAACGGTCGTAACGACGATTCTTCTCCCCAT  
 N G L L F I N T T I A S I A A K E E G V -  
 241 TCTTTGGATAAAAGAAGCCCCAAGATGGTGCAAGGGCTGGCTGCTTGGAGGAAGATG 300  
 241 AGAAACCTATTTCTCGGGGTTCTACCACGTTCCCAGACCGACGAAACCCCTCTAC  
 S L D K R S P K M V Q G S G C F G R K M -  
 301 GACCGGATCAGCTCCTCCAGTGGCCTGGGCTGCAAAGTGCTGAGGCGGCATTAA 354  
 301 CTGGCCTAGTCGAGGAGGTACCGGACCCGACGTTCACGACTCCGCCGTAAATT  
 D R I S S S S G L G C K V L R R H \* -

Fig. 14C

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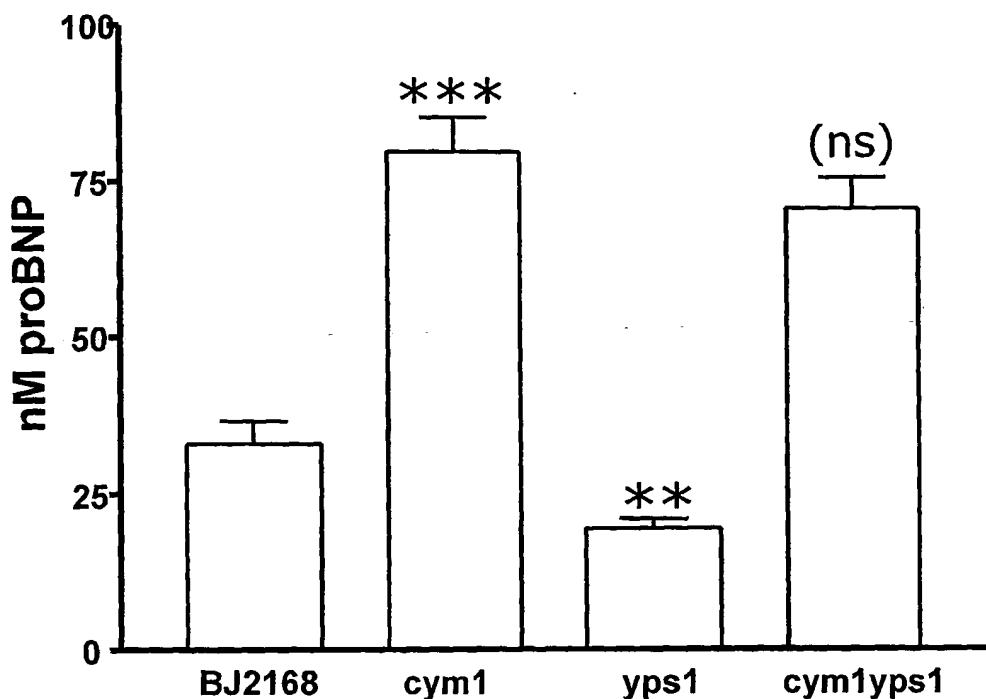


Fig. 15A

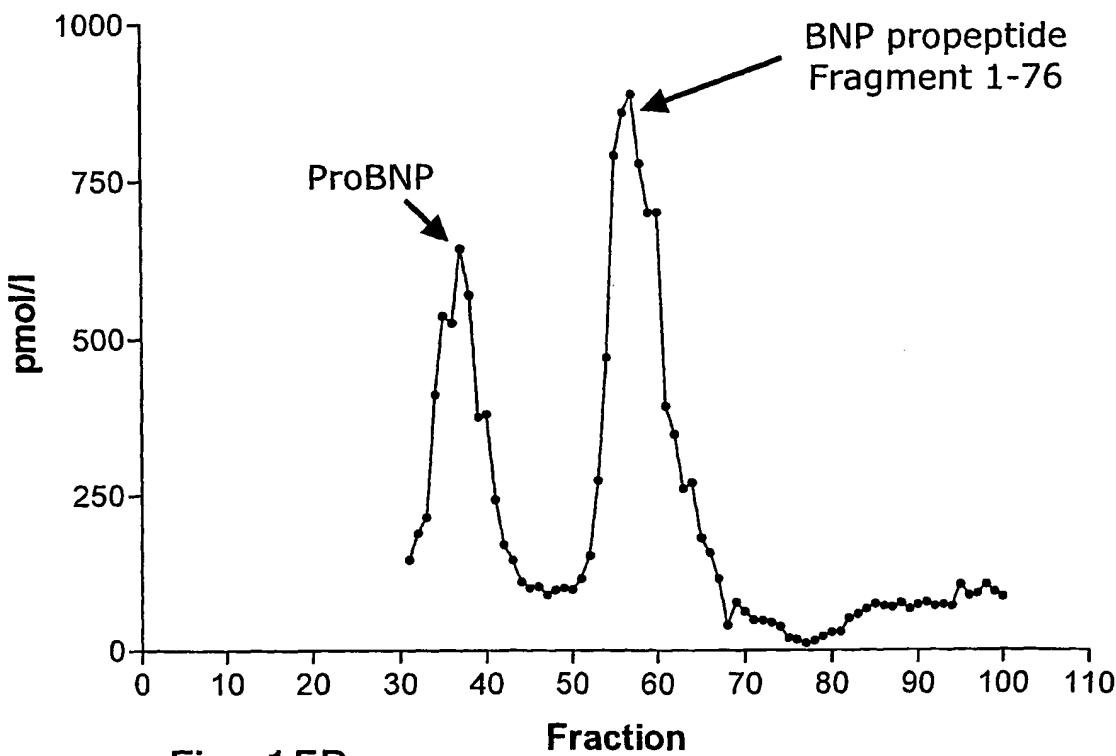


Fig. 15B